



## SEQUENCE LISTING

<110> Moon, Chulso  
Mao, Li

<120> DAP-Kinase and HOXA9, Two Human Genes Associated with Genesis,  
Progression, and Aggressiveness of Non-Small Cell Lung Cancer

<130> 10620-1U1

<140> 10/045,400  
<141> 2001-11-29

<150> US 60/250,083  
<151> 2000-11-29

<160> 7

<170> PatentIn version 3.1

<210> 1  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> HoxA9 PCR Primer

<400> 1  
ccggccttat ggcattaaac

20

<210> 2  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> HoxA9 PCR Primer

<400> 2  
agttggctgc tgggttattg

20

<210> 3  
<211> 218  
<212> DNA  
<213> Artificial

<220>  
<223> HoxA9 Probe

<400> 3  
ccggccttat ggcattaaac ctgaaccgct gtcggccaga aggggtgact gtcccacgct 60  
tgacactcac actttgtccc tgactgacta tgcttgtggt tctcctccag ttgatagaga 120  
aaaacaaccc agcgaaggcg cttctccga aaacaatgcc gagaatgaga gcggcggaga 180

## P-CAN1004sequencelisting.txt

caagcccccc atcgatccca ataacccagc agccaact 218  
 <210> 4  
 <211> 5910  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (337) .. (4632)  
 <223>  
 <400> 4  
 cggaggacag ccggaccgag ccaacgcccgg ggactttgtt ccctccacgg aggggactcg 60  
 gcaactcgca gcggcagggt ctggggccgg cgccctggag ggatctgcgc cccccactca 120  
 ctcccttagct gtgttcccgcc cgccgcccccg gctagtctcc ggccgctggcg cctatggtcg 180  
 gcctccgaca gcgatccgga gggaccgggg gagctcccgag gcccggggaa ctggagactg 240  
 atgcattgagg ggcctacgga ggccgaggag cggtggtgat ggtctggaa gcggagctga 300  
 agtccccctgg gcttttgtga ggcgtgacag tttatc atg acc gtg ttc agg cag 354  
 Met Thr Val Phe Arg Gln  
 1 5  
 gaa aac gtg gat gat tac tac gac acc ggc gag gaa ctt ggc agt gga 402  
 Glu Asn Val Asp Asp Tyr Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly  
 10 15 20  
 cag ttt gcg gtt gtg aag aaa tgc cgt gag aaa agt acc ggc ctc cag 450  
 Gln Phe Ala Val Val Lys Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln  
 25 30 35  
 tat gcc gcc aaa ttc atc aag aaa agg agg act aag tcc agc cgg cgg 498  
 Tyr Ala Ala Lys Phe Ile Lys Arg Arg Thr Lys Ser Ser Arg Arg  
 40 45 50  
 ggt gtg agc cgc gag gac atc gag cgg gag gtc agc atc ctg aag gag 546  
 Gly Val Ser Arg Glu Asp Ile Glu Arg Glu Val Ser Ile Leu Lys Glu  
 55 60 65 70  
 atc cag cac ccc aat gtc atc acc ctg cac gag gtc tat gag aac aag 594  
 Ile Gln His Pro Asn Val Ile Thr Leu His Glu Val Tyr Glu Asn Lys  
 75 80 85  
 acg gac gtc atc ctg atc ttg gaa ctc gtt gca ggt ggc gag ctg ttt 642  
 Thr Asp Val Ile Leu Ile Leu Glu Leu Val Ala Gly Gly Glu Leu Phe  
 90 95 100  
 gac ttc tta gct gaa aag gaa tct tta act gaa gag gaa gca act gaa 690  
 Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr Glu Glu Ala Thr Glu  
 105 110 115  
 ttt ctc aaa caa att ctt aat ggt gtt tac tac ctg cac tcc ctt caa 738  
 Phe Leu Lys Gln Ile Leu Asn Gly Val Tyr Tyr Leu His Ser Leu Gln  
 120 125 130

P-CAN1004sequencelisting.txt

atc gcc cac ttt gat ctt aag cct gag aac ata atg ctt ttg gat aga Ile Ala His Phe Asp Leu Lys Pro Glu Asn Ile Met Leu Leu Asp Arg 135 140 145 150	786
aat gtc ccc aaa cct cggtt gac att gac ttt ggg ttg gcc cat Asn Val Pro Lys Pro Arg Ile Lys Ile Asp Phe Gly Leu Ala His 155 160 165	834
aaa att gac ttt gga aat gaa ttt aaa aac ata ttt ggg act cca gag Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu 170 175 180	882
ttt gtc gct cct gag ata gtc aac tat gaa cct ctt ggt ctt gag gca Phe Val Ala Pro Glu Ile Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala 185 190 195	930
gat atg tgg agt atc ggg gta ata acc tat atc ctc cta agt ggg gcc Asp Met Trp Ser Ile Gly Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala 200 205 210	978
tcc cca ttt ctt gga gac act aag caa gaa acg tta gca aat gta tcc Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Val Ser 215 220 225 230	1026
gct gtc aac tac gaa ttt gag gat gaa tac ttc agt aat acc agt gcc Ala Val Asn Tyr Glu Phe Asp Glu Tyr Phe Ser Asn Thr Ser Ala 235 240 245	1074
cta gcc aaa gat ttc ata aga aga ctt ctg gtc aag gat cca aag aag Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu Val Lys Asp Pro Lys Lys 250 255 260	1122
aga atg aca att caa gat agt ttg cag cat ccc tgg atc aag cct aaa Arg Met Thr Ile Gln Asp Ser Leu Gln His Pro Trp Ile Lys Pro Lys 265 270 275	1170
gat aca caa cag gca ctt agt aga aaa gca tca gca gta aac atg gag Asp Thr Gln Gln Ala Leu Ser Arg Lys Ala Ser Ala Val Asn Met Glu 280 285 290	1218
aaa ttc aag aag ttt gca gcc cggtt aaa aaa tgg aaa caa tcc gtt cgc Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys Trp Lys Gln Ser Val Arg 295 300 305 310	1266
ttg ata tca ctg tgc caa aga tta tcc agg tca ttc ctg tcc aga agt Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg Ser Phe Leu Ser Arg Ser 315 320 325	1314
aac atg agt gtt gcc aga agc gat gat act ctg gat gag gaa gac tcc Asn Met Ser Val Ala Arg Ser Asp Asp Thr Leu Asp Glu Glu Asp Ser 330 335 340	1362
ttt gtg atg aaa gcc atc atc cat gcc atc aac gat gac aat gtc cca Phe Val Met Lys Ala Ile Ile His Ala Ile Asn Asp Asp Asn Val Pro 345 350 355	1410
ggc ctg cag cac ctt ctg ggc tca tta tcc aac tat gat gtt aac caa Gly Leu Gln His Leu Leu Gly Ser Leu Ser Asn Tyr Asp Val Asn Gln	1458

P-CAN1004sequencelisting.txt

360	365	370	
ccc aac aag cac ggg aca cct cca tta ctc att gct gct ggc tgt ggg Pro Asn Lys His Gly Thr Pro Pro Leu Leu Ile Ala Ala Gly Cys Gly 375 380 385 390			1506
aat att caa ata cta cag ttg ctc att aaa aga ggc tcg aga atc gat Asn Ile Gln Ile Leu Gln Leu Ile Lys Arg Gly Ser Arg Ile Asp 395 400 405			1554
gtc cag gat aag ggc ggg tcc aat gcc gtc tac tgg gct gct cgg cat Val Gln Asp Lys Gly Gly Ser Asn Ala Val Tyr Trp Ala Ala Arg His 410 415 420			1602
ggc cac gtc gat acc ttg aaa ttt ctc agt gag aac aaa tgc cct ttg Gly His Val Asp Thr Leu Lys Phe Leu Ser Glu Asn Lys Cys Pro Leu 425 430 435			1650
gat gtg aaa gac aag tct gga gag atg gcc ctc cac gtg gca gct cgc Asp Val Lys Asp Lys Ser Gly Glu Met Ala Leu His Val Ala Ala Arg 440 445 450			1698
tat ggc cat gct gac gtg gct caa gtt act tgt gca gct tcg gct caa Tyr Gly His Ala Asp Val Ala Gln Val Thr Cys Ala Ala Ser Ala Gln 455 460 465 470			1746
atc cca ata tcc agg aca aag gaa gaa gaa acc ccc ctg cac tgt gct Ile Pro Ile Ser Arg Thr Lys Glu Glu Thr Pro Leu His Cys Ala 475 480 485			1794
gct tgg cac ggc tat tac tct gtg gcc aaa gcc ctt tgt gaa gcc ggc Ala Trp His Gly Tyr Ser Val Ala Lys Ala Leu Cys Glu Ala Gly 490 495 500			1842
tgt aac gtg aac atc aag aac cga gaa gga gag acg ccc ctc ctg aca Cys Asn Val Asn Ile Lys Asn Arg Glu Gly Glu Thr Pro Leu Leu Thr 505 510 515			1890
gcc tct gcc agg ggc tac cac gac atc gtg gag tgt ctg gcc gaa cat Ala Ser Ala Arg Gly Tyr His Asp Ile Val Glu Cys Leu Ala Glu His 520 525 530			1938
gga gcc gac ctt aat gct tgc gac aag gac gga cac att gcc ctt cat Gly Ala Asp Leu Asn Ala Cys Asp Lys Asp Gly His Ile Ala Leu His 535 540 545 550			1986
ctg gct gta aga cgg tgt cag atg gag gta atc aag act ctc ctc agc Leu Ala Val Arg Arg Cys Gln Met Glu Val Ile Lys Thr Leu Leu Ser 555 560 565			2034
caa ggg tgt ttc gtc gat tat caa gac agg cac ggc aat act ccc ctc Gln Gly Cys Phe Val Asp Tyr Gln Asp Arg His Gly Asn Thr Pro Leu 570 575 580			2082
cat gtg gca tgt aaa gat ggc aac atg cct atc gtg gtg gcc ctc tgt His Val Ala Cys Lys Asp Gly Asn Met Pro Ile Val Val Ala Leu Cys 585 590 595			2130
gaa gca aac tgc aat ttg gac atc tcc aac aag tat ggg cga acg cct			2178

Glu Ala Asn Cys Asn Leu Asp Ile Ser Asn Lys Tyr Gly Arg Thr Pro 600 605 610	
ctg cac ctt gcg gcc aac aac gga atc cta gac gtg gtc cggtatctc Leu His Leu Ala Ala Asn Asn Gly Ile Leu Asp Val Val Arg Tyr Leu 615 620 625 630	2226
tgt ctg atg gga gcc agc gtt gag gcg ctg acc acg gac gga aag acg Cys Leu Met Gly Ala Ser Val Glu Ala Leu Thr Thr Asp Gly Lys Thr 635 640 645	2274
gca gaa gat ctt gct aga tcg gaa cag cac gag cac gta gca ggt ctc Ala Glu Asp Leu Ala Arg Ser Glu Gln His Glu His Val Ala Gly Leu 650 655 660	2322
ctt gca aga ctt cga aag gat acg cac cga gga ctc ttc atc cag cag Leu Ala Arg Leu Arg Lys Asp Thr His Arg Gly Leu Phe Ile Gln Gln 665 670 675	2370
ctc cga ccc aca cag aac ctg cag cca aga att aag ctc aag ctg ttt Leu Arg Pro Thr Gln Asn Leu Gln Pro Arg Ile Lys Leu Lys Leu Phe 680 685 690	2418
ggc cac tcg gga tcc ggg aaa acc acc ctt gta gaa tct ctc aag tgt Gly His Ser Gly Ser Gly Lys Thr Thr Leu Val Glu Ser Leu Lys Cys 695 700 705 710	2466
ggg ctg ctg agg agc ttt ttc aga agg cgt cgg ccc aga ctg tct tcc Gly Leu Leu Arg Ser Phe Phe Arg Arg Arg Pro Arg Leu Ser Ser 715 720 725	2514
acc aac tcc agc agg ttc cca cct tca ccc ctg gct tct aag ccc aca Thr Asn Ser Ser Arg Phe Pro Pro Ser Pro Leu Ala Ser Lys Pro Thr 730 735 740	2562
gtc tca gtg agc atc aac aac ctg tac cca ggc tgc gag aac gtg agt Val Ser Val Ser Ile Asn Asn Leu Tyr Pro Gly Cys Glu Asn Val Ser 745 750 755	2610
gtg agg agc cgc agc atg atg ttc gag ccg ggt ctt acc aaa ggg atg Val Arg Ser Arg Ser Met Met Phe Glu Pro Gly Leu Thr Lys Gly Met 760 765 770	2658
ctg gag gtg ttt gtg gcc ccg acc cac cac ccg cac tgc tcg gcc gat Leu Glu Val Phe Val Ala Pro Thr His His Pro His Cys Ser Ala Asp 775 780 785 790	2706
gac cag tcc acc aag gcc atc gac atc cag aac gct tat ttg aat gga Asp Gln Ser Thr Lys Ala Ile Asp Ile Gln Asn Ala Tyr Leu Asn Gly 795 800 805	2754
gtt ggc gat ttc agc gtg tgg gag ttc tct gga aat cct gtg tat ttc Val Gly Asp Phe Ser Val Trp Glu Phe Ser Gly Asn Pro Val Tyr Phe 810 815 820	2802
tgc tgt tat gac tat ttt gct gca aat gat ccc acg tca atc cat gtt Cys Cys Tyr Asp Tyr Phe Ala Ala Asn Asp Pro Thr Ser Ile His Val 825 830 835	2850

P-CAN1004sequencelisting.txt

gtt gtc ttt agt cta gaa gag ccc tat gag atc cag ctg aac cca gtg Val Val Phe Ser Leu Glu Glu Pro Tyr Glu Ile Gln Leu Asn Pro Val 840 845 850	2898
att ttc tgg ctc agt ttc ctg aag tcc ctt gtc cca gtt gaa gaa ccc Ile Phe Trp Leu Ser Phe Leu Lys Ser Leu Val Pro Val Glu Glu Pro 855 860 865 870	2946
ata gcc ttc ggt ggc aag ctg aag aac cca ctc caa gtt gtc ctg gtg Ile Ala Phe Gly Gly Lys Leu Lys Asn Pro Leu Gln Val Val Leu Val 875 880 885	2994
gcc acc cac gct gac atc atg aat gtt cct cga ccg gct gga ggc gag Ala Thr His Ala Asp Ile Met Asn Val Pro Arg Pro Ala Gly Gly Glu 890 895 900	3042
ttt gga tat gac aaa gac aca tcg ttg ctg aaa gag att agg aac agg Phe Gly Tyr Asp Lys Asp Thr Ser Leu Leu Lys Glu Ile Arg Asn Arg 905 910 915	3090
ttt gga aat gat ctt cac att tca aat aag ctg ttt gtt ctg gat gct Phe Gly Asn Asp Leu His Ile Ser Asn Lys Leu Phe Val Leu Asp Ala 920 925 930	3138
ggg gct tct ggg tca aag gac atg aag gta ctt cga aat cat ctg caa Gly Ala Ser Gly Ser Lys Asp Met Lys Val Leu Arg Asn His Leu Gln 935 940 945 950	3186
gaa ata cga agc cag att gtt tcg gtc tgt cct ccc atg act cac ctg Glu Ile Arg Ser Gln Ile Val Ser Val Cys Pro Pro Met Thr His Leu 955 960 965	3234
tgt gag aaa atc atc tcc acg ctg cct tcc tgg agg aag ctc aat gga Cys Glu Lys Ile Ile Ser Thr Leu Pro Ser Trp Arg Lys Leu Asn Gly 970 975 980	3282
ccc aac cag ctg atg tcg ctg cag cag ttt gtg tac gac gtg cag gac Pro Asn Gln Leu Met Ser Leu Gln Gln Phe Val Tyr Asp Val Gln Asp 985 990 995	3330
cag ctg aac ccc ctg gcc agc gag gag gac ctc agg cgc att gct Gln Leu Asn Pro Leu Ala Ser Glu Glu Asp Leu Arg Arg Ile Ala 1000 1005 1010	3375
cag cag ctc cac agc aca ggc gag atc aac atc atg caa agt gaa Gln Gln Leu His Ser Thr Gly Glu Ile Asn Ile Met Gln Ser Glu 1015 1020 1025	3420
aca gtt cag gac gtg ctg ctc ctg gac ccc cgc tgg ctc tgc aca Thr Val Gln Asp Val Leu Leu Leu Asp Pro Arg Trp Leu Cys Thr 1030 1035 1040	3465
aac gtc ctg ggg aag ttg ctg tcc gtg gag acc cca cgg gcg ctg Asn Val Leu Gly Lys Leu Leu Ser Val Glu Thr Pro Arg Ala Leu 1045 1050 1055	3510
cac cac tac cgg ggc cgc tac acc gtg gag gac atc cag cgc ctg His His Tyr Arg Gly Arg Tyr Thr Val Glu Asp Ile Gln Arg Leu 1060 1065 1070	3555

gtg ccc gac agc gac gtg gag gag ctg ctg cag atc ctc gat gcc	3600
Val Pro Asp Ser Asp Val Glu Glu Leu Leu Gln Ile Leu Asp Ala	
1075 1080 1085	
atg gac atc tgc gcc cg <sup>g</sup> gac ctg agc agc ggg acc atg gtg gac	3645
Met Asp Ile Cys Ala Arg Asp Leu Ser Ser Gly Thr Met Val Asp	
1090 1095 1100	
gtc cca gcc ctg atc aag aca gac aac ctg cac cgc tcc tgg gct	3690
Val Pro Ala Leu Ile Lys Thr Asp Asn Leu His Arg Ser Trp Ala	
1105 1110 1115	
gat gag gag gac gag gtg atg gtg tat ggt ggc gtg cgc atc gtg	3735
Asp Glu Glu Asp Glu Val Met Val Tyr Gly Gly Val Arg Ile Val	
1120 1125 1130	
ccc gtg gaa cac ctc acc ccc ttc cca tgt ggc atc ttt cac aag	3780
Pro Val Glu His Leu Thr Pro Phe Pro Cys Gly Ile Phe His Lys	
1135 1140 1145	
gtc cag gtg aac ctg tgc cg <sup>g</sup> tgg atc cac cag caa agc aca gag	3825
Val Gln Val Asn Leu Cys Arg Trp Ile His Gln Gln Ser Thr Glu	
1150 1155 1160	
ggc gac gc <sup>g</sup> gac atc cgc ctg tgg gtg aat ggc tgc aag ctg gcc	3870
Gly Asp Ala Asp Ile Arg Leu Trp Val Asn Gly Cys Lys Leu Ala	
1165 1170 1175	
aac cgt ggg gcc gag ctg ctg gtg ctg ctg gtc aac cac ggc cag	3915
Asn Arg Gly Ala Glu Leu Leu Val Leu Leu Val Asn His Gly Gln	
1180 1185 1190	
ggc att gag gtc cag gtc cgt ggc ctg gag acg gag aag atc aag	3960
Gly Ile Glu Val Gln Val Arg Gly Leu Glu Thr Glu Lys Ile Lys	
1195 1200 1205	
tgc tgc ctg ctg gac tcg gtg tgc agc acc att gag aac gtc	4005
Cys Cys Leu Leu Leu Asp Ser Val Cys Ser Thr Ile Glu Asn Val	
1210 1215 1220	
atg gcc acc acg ctg cca gg <sup>g</sup> ctc ctg acc gtg aag cat tac ctg	4050
Met Ala Thr Thr Leu Pro Gly Leu Leu Thr Val Lys His Tyr Leu	
1225 1230 1235	
agc ccc cag cag ctg cg <sup>g</sup> gag cac cat gag ccc gtc atg atc tac	4095
Ser Pro Gln Gln Leu Arg Glu His His Glu Pro Val Met Ile Tyr	
1240 1245 1250	
cag cca cg <sup>g</sup> gac ttc ttc cg <sup>g</sup> gca cag act ctg aag gaa acc tca	4140
Gln Pro Arg Asp Phe Phe Arg Ala Gln Thr Leu Lys Glu Thr Ser	
1255 1260 1265	
ctg acc aac acc atg ggg ggg tac aag gaa agc ttc agc agc atc	4185
Leu Thr Asn Thr Met Gly Gly Tyr Lys Glu Ser Phe Ser Ser Ile	
1270 1275 1280	
atg tgc ttc ggg tgt cac gac gtc tac tca cag gcc agc ctc ggc	4230
Met Cys Phe Gly Cys His Asp Val Tyr Ser Gln Ala Ser Leu Gly	

1285	1290	1295	
atg gac atc cat gca tca gac	ctg aac ctc ctc act	cg <sup>g</sup> agg aaa	4275
Met Asp Ile His Ala Ser Asp	Leu Asn Leu Leu Thr	Arg Arg Lys	
1300	1305	1310	
ctg agt cgc ctg ctg gac ccg	ccc gac ccc ctg ggg	aag gac tgg	4320
Leu Ser Arg Leu Leu Asp Pro	Pro Asp Pro Leu Gly	Lys Asp Trp	
1315	1320	1325	
tgc ctt ctc gcc atg aac tta	ggc ctc cct gac ctc	gtg gca aag	4365
Cys Leu Leu Ala Met Asn Leu	Gly Leu Pro Asp Leu	Val Ala Lys	
1330	1335	1340	
tac aac acc aat aac ggg gct	ccc aag gat ttc ctc	ccc agc ccc	4410
Tyr Asn Thr Asn Asn Gly Ala	Pro Lys Asp Phe Leu	Pro Ser Pro	
1345	1350	1355	
ctc cac gcc ctg ctg cg <sup>g</sup> gaa	tgg acc acc tac cct	gag agc aca	4455
Leu His Ala Leu Leu Arg Glu	Trp Thr Thr Tyr Pro	Glu Ser Thr	
1360	1365	1370	
gtg ggc acc ctc atg tcc aaa	ctg agg gag ctg ggt	cgc cg <sup>g</sup> gat	4500
Val Gly Thr Leu Met Ser Lys	Leu Arg Glu Leu Gly	Arg Arg Asp	
1375	1380	1385	
gcc gca gac ctt ttg ctg aag	gca tcc tct gtg ttc	aaa atc aac	4545
Ala Ala Asp Leu Leu Lys	Ala Ser Ser Val Phe	Lys Ile Asn	
1390	1395	1400	
ctg gat ggc aat ggc cag gag	gcc tat gcc tcg agc	tgc aac agc	4590
Leu Asp Gly Asn Gly Gln Glu	Ala Tyr Ala Ser Ser	Cys Asn Ser	
1405	1410	1415	
ggc acc tct tac aat tcc att	agc tct gtt gta tcc	cg <sup>g</sup> tga	4632
Gly Thr Ser Tyr Asn Ser Ile	Ser Ser Val Val Ser	Arg	
1420	1425	1430	
gggcagcctc tggcttggac agggtctgtt	tggactgcag aaccaagggg	gtgatgtac	4692
ccatccttcc ctttggagat gctgagggtg	tttcttcctg cacccacago	cagggggatg	4752
ccactcctcc ctccggcttg acctgtttct	ctgcccgtac ctccctcccc	gtctcattcc	4812
gttgtctgtg gatggtcatt gcagtttaag	agcagaacag atctttact	ttggccgctt	4872
gaaaagctag tgtacccct ctcagtgttt	tggactccat ctctcatcct	ccagtacctt	4932
gcttcttact gataattttg ctggaattcc	taactttca atgacatttt	ttttaactat	4992
catattgatt gtcctttaaa aaagaaaagt	gcatatttat caaaaatgtg	tatttcttat	5052
acgctttct gtgttataacc atttcctcag	cttatctctt ttatatttgt	aggagaaact	5112
cccatgtatg gaatcccact gtatgattt	taaacagaca atatgtgagt	gcctttgca	5172
gaagagggtg tgtttcaa atcggagtc	agccaggagc tgtcaccaag	gaaacgctac	5232
ctctctgtcc cttgctgtat gctgatcatac	gccagaggtg cttcaccctg	agttttgttt	5292

P-CAN1004sequencelisting.txt

tgtattgttt tctgacagtt tttctgtttt gtttggcaag gaaaggggag aagggaatcc 5352  
tcctccaggg tgattttatg atcagtgttg ttgctctagg aagacatttt tccgtttgct 5412  
tttggccaa tgtcaatgtg aacgtccaca tgaaacctac acactgtcat gtttcatcat 5472  
tccctctcat ctcaggtaga aggttgacac agttgttaggg ttacagagac ctatgtaaga 5532  
attcagaaga cccctgactc atcatttgcg gcagtcctt ataattggtg catagcagat 5592  
ggtttccaca ttttagatcct ggtttcataa cttcctgtac ttgaagtcta aaagcagaaa 5652  
ataaaaggaag caagtttct tccatgattt taaattgtga tcgagttta aattgatagg 5712  
agggAACATG tcctaattct tctgtcctga gaagcatgta atgttaatgt tatatcatat 5772  
gtatatatat atatgcacta tgtatataca tatatattaa tactggtatt tttacttaat 5832  
ctataaaatg tcgttaaaaaa gttgttgtt ttttcttt ttataaata aactgttgct 5892  
cgtaaaaaaa aaaaaaaaaa 5910

<210> 5  
<211> 1431  
<212> PRT  
<213> Homo sapiens

<400> 5

Met Thr Val Phe Arg Gln Glu Asn Val Asp Asp Tyr Tyr Asp Thr Gly  
1 5 10 15

Glu Glu Leu Gly Ser Gly Gln Phe Ala Val Val Lys Lys Cys Arg Glu  
20 25 30

Lys Ser Thr Gly Leu Gln Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg  
35 40 45

Thr Lys Ser Ser Arg Arg Gly Val Ser Arg Glu Asp Ile Glu Arg Glu  
50 55 60

Val Ser Ile Leu Lys Glu Ile Gln His Pro Asn Val Ile Thr Leu His  
65 70 75 80

Glu Val Tyr Glu Asn Lys Thr Asp Val Ile Leu Ile Leu Glu Leu Val  
85 90 95

Ala Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr  
100 105 110

Glu Glu Glu Ala Thr Glu Phe Leu Lys Gln Ile Leu Asn Gly Val Tyr  
 115 120 125

Tyr Leu His Ser Leu Gln Ile Ala His Phe Asp Leu Lys Pro Glu Asn  
 130 135 140

Ile Met Leu Leu Asp Arg Asn Val Pro Lys Pro Arg Ile Lys Ile Ile  
 145 150 155 160

Asp Phe Gly Leu Ala His Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn  
 165 170 175

Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu  
 180 185 190

Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr  
 195 200 205

Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu  
 210 215 220

Thr Leu Ala Asn Val Ser Ala Val Asn Tyr Glu Phe Glu Asp Glu Tyr  
 225 230 235 240

Phe Ser Asn Thr Ser Ala Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu  
 245 250 255

Val Lys Asp Pro Lys Lys Arg Met Thr Ile Gln Asp Ser Leu Gln His  
 260 265 270

Pro Trp Ile Lys Pro Lys Asp Thr Gln Gln Ala Leu Ser Arg Lys Ala  
 275 280 285

Ser Ala Val Asn Met Glu Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys  
 290 295 300

Trp Lys Gln Ser Val Arg Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg  
 305 310 315 320

Ser Phe Leu Ser Arg Ser Asn Met Ser Val Ala Arg Ser Asp Asp Thr  
 325 330 335

Leu Asp Glu Glu Asp Ser Phe Val Met Lys Ala Ile Ile His Ala Ile  
 340 345 350

P-CAN1004sequencelisting.txt

Asn Asp Asp Asn Val Pro Gly Leu Gln His Leu Leu Gly Ser Leu Ser  
355 360 365

Asn Tyr Asp Val Asn Gln Pro Asn Lys His Gly Thr Pro Pro Leu Leu  
370 375 380

Ile Ala Ala Gly Cys Gly Asn Ile Gln Ile Leu Gln Leu Leu Ile Lys  
385 390 395 400

Arg Gly Ser Arg Ile Asp Val Gln Asp Lys Gly Gly Ser Asn Ala Val  
405 410 415

Tyr Trp Ala Ala Arg His Gly His Val Asp Thr Leu Lys Phe Leu Ser  
420 425 430

Glu Asn Lys Cys Pro Leu Asp Val Lys Asp Lys Ser Gly Glu Met Ala  
435 440 445

Leu His Val Ala Ala Arg Tyr Gly His Ala Asp Val Ala Gln Val Thr  
450 455 460

Cys Ala Ala Ser Ala Gln Ile Pro Ile Ser Arg Thr Lys Glu Glu Glu  
465 470 475 480

Thr Pro Leu His Cys Ala Ala Trp His Gly Tyr Tyr Ser Val Ala Lys  
485 490 495

Ala Leu Cys Glu Ala Gly Cys Asn Val Asn Ile Lys Asn Arg Glu Gly  
500 505 510

Glu Thr Pro Leu Leu Thr Ala Ser Ala Arg Gly Tyr His Asp Ile Val  
515 520 525

Glu Cys Leu Ala Glu His Gly Ala Asp Leu Asn Ala Cys Asp Lys Asp  
530 535 540

Gly His Ile Ala Leu His Leu Ala Val Arg Arg Cys Gln Met Glu Val  
545 550 555 560

Ile Lys Thr Leu Leu Ser Gln Gly Cys Phe Val Asp Tyr Gln Asp Arg  
565 570 575

His Gly Asn Thr Pro Leu His Val Ala Cys Lys Asp Gly Asn Met Pro  
580 585 590

P-CAN1004sequencelisting.txt

Ile Val Val Ala Leu Cys Glu Ala Asn Cys Asn Leu Asp Ile Ser Asn  
595 600 605

Lys Tyr Gly Arg Thr Pro Leu His Leu Ala Ala Asn Asn Gly Ile Leu  
610 615 620

Asp Val Val Arg Tyr Leu Cys Leu Met Gly Ala Ser Val Glu Ala Leu  
625 630 635 640

Thr Thr Asp Gly Lys Thr Ala Glu Asp Leu Ala Arg Ser Glu Gln His  
645 650 655

Glu His Val Ala Gly Leu Leu Ala Arg Leu Arg Lys Asp Thr His Arg  
660 665 670

Gly Leu Phe Ile Gln Gln Leu Arg Pro Thr Gln Asn Leu Gln Pro Arg  
675 680 685

Ile Lys Leu Lys Leu Phe Gly His Ser Gly Ser Gly Lys Thr Thr Leu  
690 695 700

Val Glu Ser Leu Lys Cys Gly Leu Leu Arg Ser Phe Phe Arg Arg Arg  
705 710 715 720

Arg Pro Arg Leu Ser Ser Thr Asn Ser Ser Arg Phe Pro Pro Ser Pro  
725 730 735

Leu Ala Ser Lys Pro Thr Val Ser Val Ser Ile Asn Asn Leu Tyr Pro  
740 745 750

Gly Cys Glu Asn Val Ser Val Arg Ser Arg Ser Met Met Phe Glu Pro  
755 760 765

Gly Leu Thr Lys Gly Met Leu Glu Val Phe Val Ala Pro Thr His His  
770 775 780

Pro His Cys Ser Ala Asp Asp Gln Ser Thr Lys Ala Ile Asp Ile Gln  
785 790 795 800

Asn Ala Tyr Leu Asn Gly Val Gly Asp Phe Ser Val Trp Glu Phe Ser  
805 810 815

Gly Asn Pro Val Tyr Phe Cys Cys Tyr Asp Tyr Phe Ala Ala Asn Asp

## P-CAN1004sequencelisting.txt

820	825	830	
Pro Thr Ser Ile His Val Val Val Phe Ser Leu Glu Glu Pro Tyr Glu			
835	840	845	
Ile Gln Leu Asn Pro Val Ile Phe Trp Leu Ser Phe Leu Lys Ser Leu			
850	855	860	
Val Pro Val Glu Glu Pro Ile Ala Phe Gly Gly Lys Leu Lys Asn Pro			
865	870	875	880
Leu Gln Val Val Leu Val Ala Thr His Ala Asp Ile Met Asn Val Pro			
885	890	895	
Arg Pro Ala Gly Gly Glu Phe Gly Tyr Asp Lys Asp Thr Ser Leu Leu			
900	905	910	
Lys Glu Ile Arg Asn Arg Phe Gly Asn Asp Leu His Ile Ser Asn Lys			
915	920	925	
Leu Phe Val Leu Asp Ala Gly Ala Ser Gly Ser Lys Asp Met Lys Val			
930	935	940	
Leu Arg Asn His Leu Gln Glu Ile Arg Ser Gln Ile Val Ser Val Cys			
945	950	955	960
Pro Pro Met Thr His Leu Cys Glu Lys Ile Ile Ser Thr Leu Pro Ser			
965	970	975	
Trp Arg Lys Leu Asn Gly Pro Asn Gln Leu Met Ser Leu Gln Gln Phe			
980	985	990	
Val Tyr Asp Val Gln Asp Gln Leu Asn Pro Leu Ala Ser Glu Glu Asp			
995	1000	1005	
Leu Arg Arg Ile Ala Gln Gln Leu His Ser Thr Gly Glu Ile Asn			
1010	1015	1020	
Ile Met Gln Ser Glu Thr Val Gln Asp Val Leu Leu Leu Asp Pro			
1025	1030	1035	
Arg Trp Leu Cys Thr Asn Val Leu Gly Lys Leu Leu Ser Val Glu			
1040	1045	1050	

P-CAN1004sequencelisting.txt

Thr Pro Arg Ala Leu His His Tyr Arg Gly Arg Tyr Thr Val Glu  
1055 1060 1065

Asp Ile Gln Arg Leu Val Pro Asp Ser Asp Val Glu Glu Leu Leu  
1070 1075 1080

Gln Ile Leu Asp Ala Met Asp Ile Cys Ala Arg Asp Leu Ser Ser  
1085 1090 1095

Gly Thr Met Val Asp Val Pro Ala Leu Ile Lys Thr Asp Asn Leu  
1100 1105 1110

His Arg Ser Trp Ala Asp Glu Glu Asp Glu Val Met Val Tyr Gly  
1115 1120 1125

Gly Val Arg Ile Val Pro Val Glu His Leu Thr Pro Phe Pro Cys  
1130 1135 1140

Gly Ile Phe His Lys Val Gln Val Asn Leu Cys Arg Trp Ile His  
1145 1150 1155

Gln Gln Ser Thr Glu Gly Asp Ala Asp Ile Arg Leu Trp Val Asn  
1160 1165 1170

Gly Cys Lys Leu Ala Asn Arg Gly Ala Glu Leu Leu Val Leu Leu  
1175 1180 1185

Val Asn His Gly Gln Gly Ile Glu Val Gln Val Arg Gly Leu Glu  
1190 1195 1200

Thr Glu Lys Ile Lys Cys Cys Leu Leu Leu Asp Ser Val Cys Ser  
1205 1210 1215

Thr Ile Glu Asn Val Met Ala Thr Thr Leu Pro Gly Leu Leu Thr  
1220 1225 1230

Val Lys His Tyr Leu Ser Pro Gln Gln Leu Arg Glu His His Glu  
1235 1240 1245

Pro Val Met Ile Tyr Gln Pro Arg Asp Phe Phe Arg Ala Gln Thr  
1250 1255 1260

Leu Lys Glu Thr Ser Leu Thr Asn Thr Met Gly Gly Tyr Lys Glu  
1265 1270 1275

Ser Phe Ser Ser Ile Met Cys Phe Gly Cys His Asp Val Tyr Ser  
 1280 1285 1290

Gln Ala Ser Leu Gly Met Asp Ile His Ala Ser Asp Leu Asn Leu  
 1295 1300 1305

Leu Thr Arg Arg Lys Leu Ser Arg Leu Leu Asp Pro Pro Asp Pro  
 1310 1315 1320

Leu Gly Lys Asp Trp Cys Leu Leu Ala Met Asn Leu Gly Leu Pro  
 1325 1330 1335

Asp Leu Val Ala Lys Tyr Asn Thr Asn Asn Gly Ala Pro Lys Asp  
 1340 1345 1350

Phe Leu Pro Ser Pro Leu His Ala Leu Leu Arg Glu Trp Thr Thr  
 1355 1360 1365

Tyr Pro Glu Ser Thr Val Gly Thr Leu Met Ser Lys Leu Arg Glu  
 1370 1375 1380

Leu Gly Arg Arg Asp Ala Ala Asp Leu Leu Leu Lys Ala Ser Ser  
 1385 1390 1395

Val Phe Lys Ile Asn Leu Asp Gly Asn Gly Gln Glu Ala Tyr Ala  
 1400 1405 1410

Ser Ser Cys Asn Ser Gly Thr Ser Tyr Asn Ser Ile Ser Ser Val  
 1415 1420 1425

Val Ser Arg  
 1430

<210> 6  
 <211> 597  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(597)  
 <223>

<400> 6  
 atg gca ggg ttc tct cct tgg cgg cgg cgg cgg cgg agg cgg cgg  
 Met Ala Gly Phe Ser Pro Trp Arg Arg Arg Gln Arg Arg Arg Arg  
 1 5 10 15

P-CAN1004sequencelisting.txt

cg <sup>g</sup> cg <sup>g</sup> cg <sup>g</sup> g <sup>c</sup> ag <sup>g</sup> ca <sup>c</sup> g <sup>t</sup> cg <sup>g</sup> g <sup>c</sup> a <sup>c</sup> c <sup>a</sup> g <sup>a</sup> ct <sup>g</sup> g <sup>t</sup> c <sup>g</sup> g <sup>t</sup>	96
Arg Arg Arg Ala Arg His Ala Ser Arg Ala Ala Pro Glu Leu Val Gly	
20 25 30	
gat tta ggt agt ttc ctg ttg gga tcc acc ttt ctc tcg aca ggc	144
Asp Leu Gly Ser Phe Leu Leu Gly Ser Thr Phe Leu Ser Thr Gly	
35 40 45	
acg aca ctg ccc ttc att act tca gtt gaa atc gtc tcc agg tac ctc	192
Thr Thr Leu Pro Phe Ile Thr Ser Val Glu Ile Val Ser Arg Tyr Leu	
50 55 60	
tgc gcg cg <sup>g</sup> gg <sup>g</sup> tc <sup>g</sup> gg <sup>c</sup> cg <sup>c</sup> gg <sup>g</sup> cat cac gg <sup>c</sup> cct ggt cgt gg <sup>c</sup>	240
Cys Ala Arg Gly Ser Gly Arg Ala Gly His His Gly Pro Gly Arg Ala	
65 70 75 80	
agg cct g <sup>c</sup> g <sup>c</sup> gt <sup>g</sup> g <sup>c</sup> a <sup>c</sup> t <sup>c</sup> g <sup>t</sup> t <sup>c</sup> c <sup>c</sup> t <sup>c</sup> g <sup>c</sup> a <sup>c</sup> g <sup>g</sup> c <sup>c</sup> t <sup>c</sup> g <sup>t</sup> g <sup>c</sup>	288
Arg Pro Ala Val Ala Thr Ser Ala Phe Pro Ala Gln Glu Pro Arg Val	
85 90 95	
ttt ctc cgc agc gct ttg cca gcc gg <sup>c</sup> ctt tcc cct tcc acc aca	336
Phe Leu Arg Ser Ala Leu Pro Ala Gly Arg Leu Ser Pro Ser Thr Thr	
100 105 110	
cac ctc cac ctg gtc aca gca gat aac cca gca gcc aac tgg ctt cat	384
His Leu His Leu Val Thr Ala Asp Asn Pro Ala Ala Asn Trp Leu His	
115 120 125	
g <sup>c</sup> g <sup>c</sup> t <sup>c</sup> c <sup>c</sup> a <sup>c</sup> t <sup>c</sup> c <sup>c</sup> a <sup>c</sup> g <sup>g</sup> t <sup>c</sup> c <sup>c</sup> t <sup>c</sup> a <sup>c</sup> a <sup>c</sup> c <sup>c</sup> a <sup>c</sup> g <sup>g</sup> a <sup>c</sup> c <sup>c</sup>	432
Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro Tyr Thr Lys His Gln Thr	
130 135 140	
ctg gaa ctg gag aaa gag ttt ctg ttc aac atg tac ctc acc agg gac	480
Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn Met Tyr Leu Thr Arg Asp	
145 150 155 160	
cgc agg tac gag gt <sup>g</sup> g <sup>c</sup> t <sup>c</sup> a <sup>c</sup> c <sup>c</sup> t <sup>c</sup> acc gag agg cag g <sup>c</sup>	528
Arg Arg Tyr Glu Val Ala Arg Leu Leu Asn Leu Thr Glu Arg Gln Val	
165 170 175	
aag atc tgg ttc cag aac cgc agg atg aaa atg aag aaa atc aac aaa	576
Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Met Lys Lys Ile Asn Lys	
180 185 190	
gac cga gca aaa gac gag tga	597
Asp Arg Ala Lys Asp Glu	
195	

<210> 7  
<211> 198  
<212> PRT  
<213> Homo sapiens

<400> 7  
Met Ala Gly Phe Ser Pro Trp Arg Arg Arg Gln Arg Arg Arg Arg Arg Arg  
1 5 10 15

Arg Arg Arg Ala Arg His Ala Ser Arg Ala Ala Pro Glu Leu Val Gly  
 20 25 30  
 Asp Leu Gly Ser Phe Leu Leu Leu Gly Ser Thr Phe Leu Ser Thr Gly  
 35 40 45  
 Thr Thr Leu Pro Phe Ile Thr Ser Val Glu Ile Val Ser Arg Tyr Leu  
 50 55 60  
 Cys Ala Arg Gly Ser Gly Arg Ala Gly His His Gly Pro Gly Arg Ala  
 65 70 75 80  
 Arg Pro Ala Val Ala Thr Ser Ala Phe Pro Ala Gln Glu Pro Arg Val  
 85 90 95  
 Phe Leu Arg Ser Ala Leu Pro Ala Gly Arg Leu Ser Pro Ser Thr Thr  
 100 105 110  
 His Leu His Leu Val Thr Ala Asp Asn Pro Ala Ala Asn Trp Leu His  
 115 120 125  
 Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro Tyr Thr Lys His Gln Thr  
 130 135 140  
 Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn Met Tyr Leu Thr Arg Asp  
 145 150 155 160  
 Arg Arg Tyr Glu Val Ala Arg Leu Leu Asn Leu Thr Glu Arg Gln Val  
 165 170 175  
 Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Met Lys Lys Ile Asn Lys  
 180 185 190  
 Asp Arg Ala Lys Asp Glu  
 195